

Amendments to the Claims

1-77. (Cancelled)

78. (Currently Amended) A method of introgressing an allele conferring soybean cyst nematode resistance into a non-resistant soybean plant comprising

(A) crossing at least one SCN resistant soybean plant ~~bearing~~ having an rhg1 SCN resistant allele with at least one SCN sensitive soybean plant ~~bearing~~ having an rhg1 SCN sensitive allele in order to form a segregating population, wherein said at least one SCN resistant soybean plant ~~bearing~~ having said rhg1 SCN resistant allele is ~~derived from one or more soybean lines~~ selected from the group consisting of PI200499, A2869, ~~PI404198B~~ PI404198 B, PI404166, PI548988, PI507354, ~~PI438489B~~, PI84751, PI407922, PI540556 and A2069 AG4301, and SCN resistant progeny thereof.

(B) screening said segregating population with one or more nucleic acid markers to identify an rhg1 SCN resistant allele, and

(C) selecting one or more members of said segregating population having said rhg1 SCN resistant allele.

79. (Currently Amended) The method according to claim 78, wherein said one or more members of said segregating population ~~bear~~ have yellow soybeans.

80. (Previously Presented) The method according to claim 78, wherein said one or more nucleic acid markers are capable of detecting single nucleotide polymorphisms or INDEL mutations.

81. (Currently Amended) The method according to claim 78, wherein said one or more nucleic acid markers are capable of detecting one or more polymorphisms located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 45400, 45416, 45439, 45611, 45916, 45958, 46049, 46113, 47057, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, 49316, 46227, 46703, and 48881.

82. (Previously Presented) The method according to claim 80, wherein said one or more nucleic acid markers are capable of detecting single nucleotide polymorphisms.

83. (Currently Amended) The method according to claim 82, wherein said single nucleotide polymorphisms are located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 45400, 45416, 45439, 45611, 45916, 45958, 46049, 46113, 47057, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, and 49316.

84. (Previously Presented) The method according to claim 80, wherein said one or more nucleic acid markers are capable of detecting INDEL mutations.

85. (Currently Amended) The method according to claim 84, wherein said INDEL mutations are located at a position in SEQ ID NO: 2 selected from the group consisting of 46227, 46703, and 48881.

86. (Currently Amended) A method of introgressing an allele conferring soybean cyst nematode resistance into a non-resistant soybean plant comprising ~~using screening~~ one or more nucleic acid markers ~~for marker-assisted selection to select one or more~~ and selecting a soybean lines plant, wherein said allele is an rhg1 allele, ~~and~~ wherein said one or more nucleic acid markers are capable of detecting one or more single nucleotide polymorphisms, and wherein said selected soybean plant is SCN resistant,
thereby introgressing said allele into said non-resistant soybean plant.

87. (Currently Amended) The method according to claim 86, wherein said single nucleotide polymorphisms in said *rhg1* gene are located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 45400, 45416, 45439, 45611, 45916, 45958, 46049, 46113, 47057, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, and 49316.

88. (Currently Amended) The method according to claim 86, wherein said introgressing said allele into said non-resistant soybean plant results in one or more resistant progeny ~~bearing~~ having yellow soybeans.

89. (Currently Amended) A method of introgressing an allele conferring soybean cyst nematode resistance into a non-resistant soybean plant comprising ~~using~~ screening one or more nucleic acid markers ~~for marker-assisted selection to select one or more~~ and selecting a soybean lines plant, wherein said one or more nucleic acid markers are capable of detecting one or more polymorphisms located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 45400, 45416, 45439, 45611, 45916, 45958, 46049, 46113, 46227, 46703, 47057, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, 48881, and 49316, and wherein said selected soybean plant is SCN resistant,

thereby introgressing said allele into said non-resistant soybean plant.

90. (Previously Presented) The method according to claim 89, wherein said introgressing said allele into said non-resistant soybean plant results in one or more resistant progeny ~~bearing~~ having yellow soybeans.

91. (New) A method of introgressing an allele conferring soybean cyst nematode resistance into a non-resistant soybean plant comprising

(A) crossing at least one SCN resistant soybean plant having an rhg1 SCN resistant allele with at least one SCN sensitive soybean plant having an rhg1 SCN sensitive allele in order to form a segregating population, wherein said at least one SCN resistant soybean plant having said rhg1 SCN resistant allele is selected from the group consisting of PI200499, A2869, PI404198 B, PI404166, PI548988, PI507354, PI84751, PI407922, AG4301, and SCN resistant progeny thereof having an rhg1 SCN resistant allele from PI200499, A2869, PI404198 B, PI404166, PI548988, PI507354, PI84751, PI407922, and AG4301,

(B) screening said segregating population with one or more nucleic acid markers to identify an rhg1 SCN resistant allele, wherein said one or more nucleic acid markers are capable of detecting a polymorphism located at a position in SEQ ID NO: 2 between 45163 and 49573, and

(C) selecting one or more members of said segregating population having said rhg1 SCN resistant allele.

92. (New) The method according to claim 91, wherein said one or more members of said segregating population have yellow soybeans.

93. (New) The method according to claim 91, wherein said one or more nucleic acid markers are capable of detecting single nucleotide polymorphisms or INDEL mutations.

94. (New) The method according to claim 91, wherein said one or more nucleic acid markers are capable of detecting one or more polymorphisms located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 45400, 45416, 45439, 45611, 45916, 45958, 46049, 46113, 47057, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, 49316, 46227, 46703, and 48881.

95. (New) The method according to claim 91, wherein said one or more nucleic acid markers are capable of detecting single nucleotide polymorphisms.

96. (New) The method according to claim 95, wherein said single nucleotide polymorphisms are located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 45400, 45416, 45439, 45611, 45916, 45958, 46049, 46113, 47057, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, and 49316.

97. (New) The method according to claim 91, wherein said one or more nucleic acid markers are capable of detecting INDEL mutations.

98. (New) The method according to claim 97, wherein said INDEL mutations are located at a position in SEQ ID NO: 2 selected from the group consisting of 46227, 46703, and 48881.

99. (New) A method for selecting a soybean plant having an rhg1 SCN resistant allele comprising

(A) isolating nucleic acid molecules from a candidate soybean plant,

(B) screening said nucleic acid molecules with one or more nucleic acid markers capable of detecting a single nucleotide polymorphism in rhg1, wherein said single nucleotide polymorphism is correlated with the presence of an SCN resistant phenotype, and

(C) selecting said candidate soybean plant if said one or more nucleic acid markers indicate the presence of said rhg1 SCN resistant allele, thereby selecting said soybean plant having said rhg1 SCN resistant allele.

100. (New) The method according to claim 99, wherein said soybean plant having said rhg1 SCN resistant allele has yellow soybeans.

101. (New) The method according to claim 99, wherein said single nucleotide polymorphism is located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 45400, 45416, 45439, 45611, 45916, 45958, 46049, 46113, 47057, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, and 49316.

102. (New) A method for selecting a soybean plant having an rhg1 SCN resistant allele comprising

(A) isolating nucleic acid molecules from a candidate soybean plant, and

(B) determining the nucleic acid sequence of an rhg1 allele or part thereof, wherein said rhg1 allele or part thereof comprises a single nucleotide polymorphism that is correlated with the presence of an SCN resistant phenotype or an SCN sensitive phenotype, and

(C) selecting said candidate soybean plant if said nucleic acid sequence of said single nucleotide polymorphism indicates the presence of said rhg1 SCN resistant allele, thereby selecting said soybean plant having said rhg1 SCN resistant allele.

103. (New) The method according to claim 102, wherein said soybean plant having said rhg1 SCN resistant allele has yellow soybeans.

104. (New) The method according to claim 102, wherein said single nucleotide polymorphism is located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 45400, 45416, 45439, 45611, 45916, 45958, 46049, 46113, 47057, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, and 49316.

105. (New) A method for investigating the rhg1 haplotype of a soybean plant comprising

- (A) isolating nucleic acid molecules from a candidate soybean plant, and
- (B) determining the nucleic acid sequence of an rhg1 allele or part thereof, wherein said rhg1 allele or part thereof comprises a single nucleotide polymorphism that is correlated with the presence of an SCN resistant phenotype or an SCN sensitive phenotype, and
- (C) comparing said nucleic acid sequence of an rhg1 allele or part thereof with a reference sequence, thereby investigating the rhg1 haplotype of a soybean plant.

106. (New) The method according to claim 105, wherein said single nucleotide polymorphism is located at a position in SEQ ID NO: 2 selected from the group consisting of 45173, 45309, 45400, 45416, 45439, 45611, 45916, 45958, 46049, 46113, 47057, 47057, 47140, 47208, 47571, 47617, 47796, 47856, 47937, 48012, 48060, 48073, 48135, 48279, 48413, 48681, 49012, and 49316.